Package: mllrnrs (via r-universe)

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Title R6-Based ML Learners for 'mlexperiments'

Version 0.0.9

Description Enhances 'mlexperiments' <https://CRAN.R-project.org/package=mlexperiments> with additional machine learning ('ML') learners. The package provides R6-based learners for the following algorithms: 'glmnet' <https://CRAN.R-project.org/package=glmnet>, 'ranger' <https://CRAN.R-project.org/package=ranger>, 'xgboost' <https://CRAN.R-project.org/package=xgboost>, and 'lightgbm' <https://CRAN.R-project.org/package=lightgbm>. These can be used directly with the 'mlexperiments' R package.

License GPL (>= 3)

URL https://github.com/kapsner/mllrnrs

BugReports https://github.com/kapsner/mllrnrs/issues

Depends R (>= 4.1.0)

Imports data.table, kdry, mlexperiments (>= 1.0.0), R6, stats

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`LearnerGlmnet` *R6 Class to construct a Glmnet learner*

Description

The `LearnerGlmnet` class is the interface to the `glmnet` R package for use with the `mlexperiments` package.

Details

Optimization metric: Can be used with

- mlexperiments::MLTuneParameters
- mlexperiments::MLCrossValidation
- mlexperiments::MLNestedCV

Super class

`mlexperiments::MLLearnerBase` -> `LearnerGlmnet`

Methods

Public methods:

- `LearnerGlmnet$new()`
- `LearnerGlmnet$clone()`

`LearnerGlmnet$new()`**:** Create a new `LearnerGlmnet` object.

Usage:

```
LearnerGlmnet$new(metric_optimization_higher_better)
```

Arguments:

`metric_optimization_higher_better` A logical. Defines the direction of the optimization metric used throughout the hyperparameter optimization.

Returns: A new `LearnerGlmnet` R6 object.

Examples:

```
if (requireNamespace("glmnet", quietly = TRUE)) {
  LearnerGlmnet$new(metric_optimization_higher_better = FALSE)
}
```

`LearnerGlmnet$clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
LearnerGlmnet$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

`glmnet::glmnet()`, `glmnet::cv.glmnet()`

Examples

```
# binary classification
if (requireNamespace("glmnet", quietly = TRUE) &&
requireNamespace("mlbench", quietly = TRUE) &&
requireNamespace("measures", quietly = TRUE)) {

  library(mlbench)
  data("BreastCancer")
  dataset <- BreastCancer |>
    data.table::as.data.table() |>
    na.omit()
  feature_cols <- colnames(dataset)[2:10]
  seed <- 123

  train_x <- model.matrix(
    ~ -1 + .,
    dataset[, .SD, .SDcols = feature_cols]
  )
  train_y <- as.integer(dataset[, get("Class")]) - 1L

  fold_list <- splitTools::create_folds(
    y = train_y,
    k = 3,
    type = "stratified",
    seed = seed
  )
  glmnet_cv <- mlexperiments::MLCrossValidation$new(
    learner = mllrnrs::LearnerGlmnet$new(
      metric_optimization_higher_better = FALSE
    ),
    fold_list = fold_list,
    ncores = 2,
    seed = 123
```

```
  )
  glmnet_cv$learner_args <- list(
    alpha = 1,
    lambda = 0.1,
    family = "binomial",
    type.measure = "class",
    standardize = TRUE
  )
  glmnet_cv$predict_args <- list(type = "response")
  glmnet_cv$performance_metric_args <- list(positive = "1", negative = "0")
  glmnet_cv$performance_metric <- mlexperiments::metric("AUC")

  # set data
  glmnet_cv$set_data(
    x = train_x,
    y = train_y
  )

  glmnet_cv$execute()
}

## ------------------------------------------------
## Method `LearnerGlmnet$new()`
## ------------------------------------------------

if (requireNamespace("glmnet", quietly = TRUE)) {
  LearnerGlmnet$new(metric_optimization_higher_better = FALSE)
}
```

`LearnerLightgbm` *R6 Class to construct a LightGBM learner*

Description

The `LearnerLightgbm` class is the interface to the `lightgbm` R package for use with the `mlexperiments` package.

Details

Optimization metric: needs to be specified with the learner parameter `metric`. The following options can be set via `options()`:

- "mlexperiments.optim.lgb.nrounds" (default: `5000L`)
- "mlexperiments.optim.lgb.early_stopping_rounds" (default: `500L`)
- "mlexperiments.lgb.print_every_n" (default: `50L`)
- "mlexperiments.lgb.verbose" (default: `-1L`)

`LearnerLightgbm` can be used with

- mlexperiments::MLTuneParameters
- mlexperiments::MLCrossValidation
- mlexperiments::MLNestedCV

Super class

`mlexperiments::MLLearnerBase` -> `LearnerLightgbm`

Methods

Public methods:

- `LearnerLightgbm$new()`
- `LearnerLightgbm$clone()`

`LearnerLightgbm$new()`: Create a new `LearnerLightgbm` object.

Usage:

```
LearnerLightgbm$new(metric_optimization_higher_better)
```

Arguments:

`metric_optimization_higher_better` A logical. Defines the direction of the optimization metric used throughout the hyperparameter optimization.

Returns: A new `LearnerLightgbm` R6 object.

Examples:

```
if (requireNamespace("lightgbm", quietly = TRUE)) {
  LearnerLightgbm$new(metric_optimization_higher_better = FALSE)
}
```

`LearnerLightgbm$clone()`: The objects of this class are cloneable with this method.

Usage:

```
LearnerLightgbm$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

`lightgbm::lgb.train()`, `lightgbm::lgb.cv()`

Examples

```
# binary classification
if (requireNamespace("lightgbm", quietly = TRUE) &&
requireNamespace("mlbench", quietly = TRUE) &&
requireNamespace("measures", quietly = TRUE)) {

  Sys.setenv("OMP_THREAD_LIMIT" = 2)

  library(mlbench)
```

```
data("BreastCancer")
dataset <- BreastCancer |>
  data.table::as.data.table() |>
  na.omit()
feature_cols <- colnames(dataset)[2:10]
seed <- 123

param_list_lightgbm <- expand.grid(
  bagging_fraction = seq(0.6, 1, .2),
  feature_fraction = seq(0.6, 1, .2),
  min_data_in_leaf = seq(10, 50, 10),
  learning_rate = seq(0.1, 0.2, 0.1),
  num_leaves = seq(10, 50, 10),
  max_depth = -1L
)

train_x <- model.matrix(
  ~ -1 + .,
  dataset[, .SD, .SDcols = feature_cols]
)
train_y <- as.integer(dataset[, get("Class")]) - 1L

fold_list <- splitTools::create_folds(
  y = train_y,
  k = 3,
  type = "stratified",
  seed = seed
)
lightgbm_cv <- mlexperiments::MLCrossValidation$new(
  learner = mllrnrs::LearnerLightgbm$new(
    metric_optimization_higher_better = FALSE
  ),
  fold_list = fold_list,
  ncores = 2,
  seed = 123
)
lightgbm_cv$learner_args <- c(
  as.list(
    data.table::data.table(
      param_list_lightgbm[37, ],
      stringsAsFactors = FALSE
    ),
  ),
  list(
    objective = "binary",
    metric = "binary_logloss"
  ),
  nrounds = 45L
)
lightgbm_cv$performance_metric_args <- list(positive = "1", negative = "0")
lightgbm_cv$performance_metric <- mlexperiments::metric("AUC")

# set data
```

```
  lightgbm_cv$set_data(
    x = train_x,
    y = train_y
  )
  # for some reason, this uses more than 2 cores on cran checks
  #lightgbm_cv$execute()
}


## ------------------------------------------------
## Method `LearnerLightgbm$new()`
## ------------------------------------------------

if (requireNamespace("lightgbm", quietly = TRUE)) {
  LearnerLightgbm$new(metric_optimization_higher_better = FALSE)
}
```

LearnerRanger *R6 Class to construct a Ranger learner*

Description

The LearnerRanger class is the interface to the ranger R package for use with the mlexperiments package.

Details

Optimization metric:

- classification: classification error rate
- regression: mean squared error Can be used with
- mlexperiments::MLTuneParameters
- mlexperiments::MLCrossValidation
- mlexperiments::MLNestedCV

Super class

mlexperiments::MLLearnerBase -> LearnerRanger

Methods

Public methods:

- LearnerRanger$new()
- LearnerRanger$clone()

LearnerRanger$new(): Create a new LearnerRanger object.

Usage:

```
LearnerRanger$new()
```

Returns: A new `LearnerRanger` R6 object.

Examples:

```
if (requireNamespace("ranger", quietly = TRUE)) {
  LearnerRanger$new()
}
```

`LearnerRanger$clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
LearnerRanger$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

`ranger::ranger()`

Examples

```
# binary classification
if (requireNamespace("ranger", quietly = TRUE) &&
requireNamespace("mlbench", quietly = TRUE) &&
requireNamespace("measures", quietly = TRUE)) {

  Sys.setenv("OMP_THREAD_LIMIT" = 2)

  library(mlbench)
  data("BreastCancer")
  dataset <- BreastCancer |>
    data.table::as.data.table() |>
    na.omit()
  feature_cols <- colnames(dataset)[2:10]
  seed <- 123

  param_list_ranger <- expand.grid(
    num.trees = seq(500, 1000, 500),
    mtry = seq(2, 6, 2),
    min.node.size = seq(1, 9, 4),
    max.depth = seq(1, 9, 4),
    sample.fraction = seq(0.5, 0.8, 0.3)
  )

  train_x <- model.matrix(
    ~ -1 + .,
    dataset[, .SD, .SDcols = feature_cols]
  )
  train_y <- as.integer(dataset[, get("Class")]) - 1L
```

```
  fold_list <- splitTools::create_folds(
    y = train_y,
    k = 3,
    type = "stratified",
    seed = seed
  )
  ranger_cv <- mlexperiments::MLCrossValidation$new(
    learner = mllrnrs::LearnerRanger$new(),
    fold_list = fold_list,
    ncores = 2,
    seed = 123
  )
  ranger_cv$learner_args <- c(
    as.list(
      data.table::data.table(
        param_list_ranger[37, ],
        stringsAsFactors = FALSE
      ),
    ),
    list(classification = TRUE)
  )
  ranger_cv$performance_metric_args <- list(positive = "1", negative = "0")
  ranger_cv$performance_metric <- mlexperiments::metric("AUC")

  # set data
  ranger_cv$set_data(
    x = train_x,
    y = train_y
  )

  ranger_cv$execute()
}


## ------------------------------------------------
## Method `LearnerRanger$new()`
## ------------------------------------------------

if (requireNamespace("ranger", quietly = TRUE)) {
  LearnerRanger$new()
}
```

LearnerXgboost *R6 Class to construct a Xgboost learner*

Description

The LearnerXgboost class is the interface to the xgboost R package for use with the mlexperiments package.

Details

Optimization metric: needs to be specified with the learner parameter `eval_metric`. The following options can be set via `options()`:

- "mlexperiments.optim.xgb.nrounds" (default: `5000L`)
- "mlexperiments.optim.xgb.early_stopping_rounds" (default: `500L`)
- "mlexperiments.xgb.print_every_n" (default: `50L`)
- "mlexperiments.xgb.verbose" (default: `FALSE`)

`LearnerXgboost` can be used with

- mlexperiments::MLTuneParameters
- mlexperiments::MLCrossValidation
- mlexperiments::MLNestedCV

Super class

`mlexperiments::MLLearnerBase` -> `LearnerXgboost`

Methods

Public methods:

- `LearnerXgboost$new()`
- `LearnerXgboost$clone()`

`LearnerXgboost$new()`: Create a new `LearnerXgboost` object.

Usage:

```
LearnerXgboost$new(metric_optimization_higher_better)
```

Arguments:

`metric_optimization_higher_better` A logical. Defines the direction of the optimization metric used throughout the hyperparameter optimization.

Returns: A new `LearnerXgboost` R6 object.

Examples:

```
if (requireNamespace("xgboost", quietly = TRUE)) {
  LearnerXgboost$new(metric_optimization_higher_better = FALSE)
}
```

`LearnerXgboost$clone()`: The objects of this class are cloneable with this method.

Usage:

```
LearnerXgboost$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

`xgboost::xgb.train()`, `xgboost::xgb.cv()`

Examples

```
if (requireNamespace("xgboost", quietly = TRUE) &&
requireNamespace("mlbench", quietly = TRUE) &&
requireNamespace("measures", quietly = TRUE)) {

  # binary classification
  Sys.setenv("OMP_THREAD_LIMIT" = 2)
  Sys.setenv("Ncpu" = 2)

  library(mlbench)
  data("BreastCancer")
  dataset <- BreastCancer |>
    data.table::as.data.table() |>
    na.omit()
  feature_cols <- colnames(dataset)[2:10]
  seed <- 123

  param_list_xgboost <- expand.grid(
     subsample = seq(0.6, 1, .2),
     colsample_bytree = seq(0.6, 1, .2),
     min_child_weight = seq(1, 5, 4),
     learning_rate = seq(0.1, 0.2, 0.1),
     max_depth = seq(1, 5, 4),
     nthread = 2
  )

  train_x <- model.matrix(
    ~ -1 + .,
    dataset[, .SD, .SDcols = feature_cols]
  )
  train_y <- as.integer(dataset[, get("Class")]) - 1L

  fold_list <- splitTools::create_folds(
    y = train_y,
    k = 3,
    type = "stratified",
    seed = seed
  )
  xgboost_cv <- mlexperiments::MLCrossValidation$new(
    learner = mllrnrs::LearnerXgboost$new(
      metric_optimization_higher_better = FALSE
    ),
    fold_list = fold_list,
    ncores = 2L,
    seed = 123
  )
  xgboost_cv$learner_args <- c(
    as.list(
      data.table::data.table(
        param_list_xgboost[37, ],
        stringsAsFactors = FALSE
      ),
```

```
    ),
    list(
      objective = "binary:logistic",
      eval_metric = "logloss"
    ),
    nrounds = 45L
  )
  xgboost_cv$performance_metric_args <- list(positive = "1", negative = "0")
  xgboost_cv$performance_metric <- mlexperiments::metric("AUC")

  # set data
  xgboost_cv$set_data(
    x = train_x,
    y = train_y
  )

  # for some reason, this uses more than 2 cores on cran checks
  #xgboost_cv$execute()
}


## ------------------------------------------------
## Method `LearnerXgboost$new()`
## ------------------------------------------------

if (requireNamespace("xgboost", quietly = TRUE)) {
  LearnerXgboost$new(metric_optimization_higher_better = FALSE)
}
```

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